

SEQUENCE LISTING

<110> Rosen, Craig A.
Haseltine, William A.

<120> Albumin Fusion Proteins

<130> PF544

<140> Unassigned

<141> 2001-04-12

<150> 60/229,358
<151> 2000-04-12

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<151> 2000-12-21

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<170> PatentIn Ver. 2.1

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<223> first 5 amino acids of mature human serum albumin

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Ile Ser Ala Asp Ala His Lys Ser
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62

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Asp	Ala	His	Lys	Ser	Glu	Val	Ala	His	Arg	Phe	Lys	Asp	Leu	Gly	Glu			
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Glu	Asn	Phe	Lys	Ala	Leu	Val	Leu	Ile	Ala	Phe	Ala	Gln	Tyr	Leu	Gln			
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Gln	Cys	Pro	Phe	Glu	Asp	His	Val	Lys	Leu	Val	Asn	Glu	Val	Thr	Glu			
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ttt gca aaa aca tgt gtt gct gat gag tca gct gaa aat tgt gac aaa 192																		
Phe	Ala	Lys	Thr	Cys	Val	Ala	Asp	Glu	Ser	Ala	Glu	Asn	Cys	Asp	Lys			
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Ser	Leu	His	Thr	Leu	Phe	Gly	Asp	Lys	Leu	Cys	Thr	Val	Ala	Thr	Leu			
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cgt gaa acc tat ggt gaa atg gct gac tgc tgt gca aaa caa gaa cct 288																		
Arg	Glu	Thr	Tyr	Gly	Glu	Met	Ala	Asp	Cys	Cys	Ala	Lys	Gln	Glu	Pro			
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gag aga aat gaa tgc ttc ttg caa cac aaa gat gac aac cca aac ctc 336																		
Glu	Arg	Asn	Glu	Cys	Phe	Leu	Gln	His	Lys	Asp	Asp	Asn	Pro	Asn	Leu			
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ccc cga ttg gtg aga cca gag gtt gat gtg atg tgc act gct ttt cat 384																		
Pro	Arg	Leu	Val	Arg	Pro	Glu	Val	Asp	Val	Met	Cys	Thr	Ala	Phe	His			
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gac aat gaa gag aca ttt ttg aaa aaa tac tta tat gaa att gcc aga Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg 130 135 140	432
aga cat cct tac ttt tat gcc ccg gaa ctc ctt ttc ttt gct aaa agg Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg 145 150 155 160	480
tat aaa gct gct ttt aca gaa tgt tgc caa gct gct gat aaa gct gcc Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala 165 170 175	528
tgc ctg ttg cca aag ctc gat gaa ctt cgg gat gaa ggg aag gct tcg Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser 180 185 190	576
tct gcc aaa cag aga ctc aaa tgt gcc agt ctc caa aaa ttt gga gaa Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu 195 200 205	624
aga gct ttc aaa gca tgg gca gtg gct cgc ctg agc cag aga ttt ccc Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro 210 215 220	672
aaa gct gag ttt gca gaa gtt tcc aag tta gtg aca gat ctt acc aaa Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys 225 230 235 240	720
gtc cac acg gaa tgc tgc cat gga gat ctg ctt gaa tgt gct gat gac Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp 245 250 255	768
agg gcg gac ctt gcc aag tat atc tgt gaa aat cag gat tcg atc tcc Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser 260 265 270	816
agt aaa ctg aag gaa tgc tgt gaa aaa cct ctg ttg gaa aaa tcc cac Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His 275 280 285	864
tgc att gcc gaa gtg gaa aat gat gag atg cct gct gac ttg cct tca Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser 290 295 300	912
tta gct gct gat ttt gtt gaa agt aag gat gtt tgc aaa aac tat gct Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala 305 310 315 320	960
gag gca aag gat gtc ttc ctg ggc atg ttt ttg tat gaa tat gca aga Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg 325 330 335	1008
agg cat cct gat tac tct gtc gtg ctg ctg ctg aga ctt gcc aag aca Arg His Pro Asp Tyr Ser Val Val Leu Leu Arg Leu Ala Lys Thr 340 345 350	1056
tat gaa acc act cta gag aag tgc tgt gcc gct gca gat cct cat gaa Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu 355 360 365	1104

tgc Cys	tat Tyr	gcc Ala	aaa Lys	gtg Val	ttc Phe	gat Asp	gaa Glu	ttt Phe	aaa Lys	cct Pro	ctt Leu	gtg Val	gaa Glu	gag Glu	cct Pro	1152
370						375										
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gtg Val	ggc Gly	agc Ser	aaa Lys	tgt Cys	tgt Cys	aaa Lys	cat His	cct Pro	gaa Glu	gca Ala	aaa Lys	aga Arg	atg Met	ccc Pro	tgt Cys	1344
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ttg Leu	gtg Val	aac Asn	agg Arg	cga Arg	cca Pro	tgc Cys	ttt Phe	tca Ser	gct Arg	ctg Leu	gaa Glu	gtc Val	gat Asp	gaa Glu	aca Thr	1488
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tac Tyr	gtt Val	ccc Pro	aaa Lys	gag Glu	ttt Phe	aat Asn	gct Ala	gaa Glu	aca Thr	ttc Phe	acc Thr	ttc Phe	cat His	gca Ala	gat Asp	1536
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 35 40 45
 Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
 50 55 60
 Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
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 Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
 85 90 95
 Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
 100 105 110
 Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
 115 120 125
 Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
 130 135 140
 Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
 145 150 155 160
 Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
 165 170 175
 Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
 180 185 190
 Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
 195 200 205
 Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
 210 215 220
 Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys
 225 230 235 240
 Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
 245 250 255
 Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
 260 265 270
 Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
 275 280 285
 Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
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 325 330 335
 Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
 340 345 350
 Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
 355 360 365
 Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
 370 375 380
 Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
 385 390 395 400
 Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
 405 410 415
 Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
 420 425 430
 Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
 435 440 445
 Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
 450 455 460
 Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
 465 470 475 480
 Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
 485 490 495
 Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
 500 505 510
 Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
 515 520 525
 Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
 530 535 540
 Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
 545 550 555 560
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0907-1700

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<223> n equals a, t, g, or c

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32

<213> Artificial Sequence

<223> reverse primer useful for generation of albumin fusion protein in which the albumin moiety is N-terminal of the Therapeutic Protein

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<220>
<223> forward primer useful for generation of albumin fusion
protein in which the albumin moiety is c-terminal of the
Therapeutic Protein

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<223> reverse primer useful for generation of albumin
fusion protein in which the albumin moiety is c-terminal of
the Therapeutic Protein

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 Tyr Ser Arg Ser Leu Asp Lys Arg
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 <223> Kozak sequence

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<223> cds natural signal sequence of human serum albumin

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<223> XhoI restriction site

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<222> (98)..(114)
<223> cds first six amino acids of human serum albumin

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PC4:HSA albumin fusion VECTOR

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<210> 32

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<211> 46
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Ala

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<212> PRT

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1 5 10 15

Trp Ala Pro Ala Arg Gly
20